Amendments to the Specification

Please amend the paragraph in Example 1, beginning on line 18 of page 26 and bridging to page 27, line 8 of the specification as follows:

Resuspended cells (approximately 10^6) were aliquoted into12x75 mm Flow Cytometry tubes and repelleted at 500 x g for 5 minutes. The HBSS was removed and 25 mL of the following antibodies (all obtained from Becton Dickenson), alone or in combination, were placed into each tube: mouse IgG1k FITC or -PE (clone MOPC 21) CD49c-PE (cl. C3II.1), CD90-FITC (cl. 5E10), CD45-FITC or -PE (cl. HI30). Tubes were gently vortexed and incubated for 30 minutes at 4°C. Cells were then washed in HBSS/1% bovine serum albumin, centrifuged (30 min, 4°C) and the resulting cellular pellet fixed by the addition of 250 microliters of 2% paraformaldhyde/HBSS. Flow cytometric analysis was performed employing a Becton Dickenson FACSVantage SE cytometer and analyzed using CELLQUEST® software. Figure 1 depicts results representing data collected from 2,500-10,000 events per panel. After compensation for non specific antibody staining using mouse IgG1 isotype controls, cellular expression of CD45, CD49c and CD90 in the cultured bone marrow cells was assessed. The adherent population derived from mononuclear cells initially purified using ammonium chloride lysis contained approximately 70% CD49c positive cells at a similar stage of culture (Figure 1A). The majority of cells that did not express CD49c were positive for expression of hematopoetic/myeloid lineage marker CD45 (Figure 1A, LR quadrant), demonstrating that the CD49c positive cell population derived from human bone marrow isolated was not directly related to known hematopoietic precursors. More than 94% of the adherent population was CD90 and CD49c positive (Figure 1B).

Please amend the paragraph in Example 2, beginning on line 27 of page 27 and bridging to line 6 of page 28 of the specification as follows:

Cytometry analysis of the CFU generated showed that approximately 50% of the adherent population expressed the marker CD49c at 7 days in vitro (Figure 2A, sum of UL and UR quadrants). The majority of cells that did not express CD49c were positive for expression of hematopoetic/myeloid lineage marker CD45 (Figure 2A, LR quadrant), demonstrating that the CD49c positive cell population derived from human bone marrow isolated by this procedure was not directly related to known hematopoietic precursors. More than 91% of the adherent population was CD90 and CD49c positive (Figure 2B).

Please amend the paragraph in Example 3, beginning on line 22 of page 28 of the specification as follows:

The purity of the cells (percentage of cells which co-express CD49c/CD90) in the Master Cell Bank was determined by flow cytometry ***using the same method as above.*** ~~More than 94% of the adherent population was CD90 and CD49c positive (Figure 1B).~~ The vast majority (>98%) of the resulting population expressed CD49c (Figure 1C) and virtually lacked any expression of the myeloid related marker CD45 (Figure 1C, LR quadrant). Thus, the expansion procedure as described herein produces a substantially homogenous population of adherent cells which co-express CD49c and CD90 and lack significant expression of the marker CD45.

Please amend the paragraph in Example 3, beginning on line 1 of page 29 of the specification as follows:

Similarly, the master cell bank generated from the CFU derived using the method of Example 2 showed that ~~more than 91% of the adherent population was CD90 and CD49c positive (Figure 2B) and~~ the majority of cells (>98.8%) of the resulting cell population expressed CD49c (Figure 2C) and virtually lacked any expression of the myeloid-related

marker CD45 (Figure 2C, LR quadrant). Thus, the expansion procedure as described herein generates a substantially homogenous population of adherent cells which co-express CD49c and CD90 and lack significant expression of the marker CD45.